



## **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/624,619  
Source: Q1PE  
Date Processed by STIC: 7/31/2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

**<http://www.uspto.gov/web/offices/pac/checker>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/efb/efs/downloads/documents.htm>**), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003



OIKE

## RAW SEQUENCE LISTING

DATE: 07/31/2003

PATENT APPLICATION: US/10/624,619

TIME: 08:01:13

Input Set : A:\0875CSEQUENCE LISTING.txt

Output Set: N:\CRF4\07312003\J624619.raw

4 <110> APPLICANT: Duvick, Jonathan P.  
 5 Gilliam, Jacob T.  
 6 Maddox, Joyce R.  
 7 Crasta, Oswald R.  
 8 Folkerts, Otto  
 11 <120> TITLE OF INVENTION: Amino Polyol Amine Oxidase  
 12 Polynucleotides and Related Polypeptides and Methods of Use  
 15 <130> FILE REFERENCE: 0875C  
 C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/624,619  
 C--> 17 <141> CURRENT FILING DATE: 2003-07-22  
 17 <150> PRIOR APPLICATION NUMBER: US 60/092,936  
 18 <151> PRIOR FILING DATE: 1998-07-15  
 20 <150> PRIOR APPLICATION NUMBER: US 09/352,168  
 21 <151> PRIOR FILING DATE: 1999-07-12  
 23 <160> NUMBER OF SEQ ID NOS: 33  
 25 <170> SOFTWARE: FastSEQ for Windows Version 3.0

## ERRORED SEQUENCES

3641 <210> SEQ ID NO: 32  
 3642 <211> LENGTH: 2490  
 3643 <212> TYPE: DNA  
 3644 <213> ORGANISM: Unknown  
 3646 <220> FEATURE:  
 3647 <223> OTHER INFORMATION: GST:glyc(-)APAO open reading frame, 2490 nt; GST  
 3648 and linker, nt 1-687; Glyc (-) APAO, nt 688-2490;  
 3649 mutation in putative glycosylation sites in bold  
 3650 and underlined, nt 1288-1290 (AAT->TCC) and nt  
 E-> ~~3651 <223> 1303-1305 (AGC->AAC) -> move over (DO NOT use TAB codes)~~ insert  
 W--> 3653 <221> NAME/KEY: CDS  
 3654 <222> LOCATION: (1)...(2487)  
 W--> 3656 <221> misc feature  
 3657 <222> LOCATION: (1)...(687)  
 3658 <223> OTHER INFORMATION: GST and linker  
 W--> 3660 <221> misc feature  
 3661 <222> LOCATION: (688)...(2490)  
 3662 <223> OTHER INFORMATION: Glyc (-) APAO  
 W--> 3664 <221> mutation  
 3665 <222> LOCATION: (1288)...(1290)  
 3666 <223> OTHER INFORMATION: mutation in putative glycosylation site (AAT->TCC)  
 W--> 3668 <221> mutation  
 3669 <222> LOCATION: (1303)...(1305)

Does Not Comply  
 Corrected Diskette Needed

Per 1.823 of Sequence Rules, 4 lines MAXIMUM

Insert  
 another <220>  
 after 4th  
 line, and  
 add a <223>  
 to beginning of  
 5th line

Please edit seqs.  
 20 and 30, too.

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3670 <223> OTHER INFORMATION: mutation in putative glycosylation site (AGC->AAC)

W--> 3672 <400> 32

3673	atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc	48
3674	Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro	
3675	1 5 10 15	
3677	act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
3678	Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
3679	20 25 30	
3681	tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
3682	Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
3683	35 40 45	
3685	ggg ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa	192
3686	Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
3687	50 55 60	
3689	tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	240
3690	Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
3691	65 70 75 80	
3693	atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa	288
3694	Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
3695	85 90 95	
3697	gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt	336
3698	Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
3699	100 105 110	
3701	aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa	384
3702	Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
3703	115 120 125	
3705	atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat	432
3706	Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
3707	130 135 140	
3709	ggg gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat	480
3710	Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
3711	145 150 155 160	
3713	gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta	528
3714	Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
3715	165 170 175	
3717	gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac	576
3718	Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
3719	180 185 190	
3721	ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc	624
3722	Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
3723	195 200 205	
3725	acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt	672
3726	Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
3727	210 215 220	
3729	gga tcc ccg gaa ttc atg gca ctt gca ccg agc tac atc aat ccc cca	720
3730	Gly Ser Pro Glu Phe Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro	
3731	225 230 235 240	
3733	aac gtc gcc tcc cca gca ggg tat tct cac gtc ggc gta ggc cca gac	768
3734	Asn Val Ala Ser Pro Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp	

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3735		245		250		255		
3737	gga ggg agg tat	gtg aca ata gct	gga cag att gga	caa gac gct tcg		816		
3738	Gly Gly Arg Tyr	Val Thr Ile Ala	Gly Gln Ile Gly	Gln Asp Ala Ser				
3739		260		265		270		
3741	ggc gtg aca gac	cct gcc tac gag	aaa cag gtt gcc	caa gca ttc gcc		864		
3742	Gly Val Thr Asp	Pro Ala Tyr Glu	Lys Gln Val Ala	Gln Ala Phe Ala				
3743		275		280		285		
3745	aat ctg cga gct	tgc ctt gct gca	gtt gga gcc act	tca aac gac gtc		912		
3746	Asn Leu Arg Ala	Cys Leu Ala Ala	Val Gly Ala Thr	Ser Asn Asp Val				
3747		290		295		300		
3749	acc aag ctc aat	tac tac atc gtc	gac tac gcc ccg	agc aaa ctc acc		960		
3750	Thr Lys Leu Asn	Tyr Tyr Ile Val	Asp Tyr Ala Pro	Ser Lys Leu Thr				
3751		305		310		315		320
3753	gca att gga gat	ggg ctg aag gct	acc ttt gcc ctt	gac agg ctc cct		1008		
3754	Ala Ile Gly Asp	Gly Leu Lys Ala	Thr Phe Ala Leu	Asp Arg Leu Pro				
3755		325		330		335		
3757	cct tgc acg ctg	gtg cca gtg tgc	gcc ttg tct tca	cct gaa tac ctc		1056		
3758	Pro Cys Thr Leu	Val Pro Val Ser	Ala Leu Ser Ser	Pro Glu Tyr Leu				
3759		340		345		350		
3761	ttt gag gtt gat	gcc acg gcg ctg	gtg ccg gga cac	acg acc cca gac		1104		
3762	Phe Glu Val Asp	Ala Thr Ala Leu	Val Pro Gly His	Thr Thr Pro Asp				
3763		355		360		365		
3765	aac gtt gcg gac	gtg gta gtg gtg	ggc gct ggc ttg	agc ggt ttg gag		1152		
3766	Asn Val Ala Asp	Val Val Val Val	Gly Ala Gly Leu	Ser Gly Leu Glu				
3767		370		375		380		
3769	acg gca cgc aaa	gtc cag gcc gcc	ggt ctg tcc tgc	ctc gtt ctt gag		1200		
3770	Thr Ala Arg Lys	Val Gln Ala Ala	Gly Leu Ser Cys	Leu Val Leu Glu				
3771		385		390		395		400
3773	gcg atg gat cgt	gta ggg gga aag	act ctg agc gta	caa tcg ggt ccc		1248		
3774	Ala Met Asp Arg	Val Gly Gly Lys	Thr Leu Ser Val	Gln Ser Gly Pro				
3775		405		410		415		
3777	ggc agg acg act	atc aac gac ctc	ggc gct gcg tgg	atc tcg gac agc		1296		
3778	Gly Arg Thr Thr	Ile Asn Asp Leu	Gly Ala Ala Trp	Ile Ser Asp Ser				
3779		420		425		430		
3781	aac caa aac gaa	gta tcc aga ttg	ttt gaa aga ttt	cat ttg gag ggc		1344		
3782	Asn Gln Asn Glu	Val Ser Arg Leu	Phe Glu Arg Phe	His Leu Glu Gly				
3783		435		440		445		
3785	gag ctc cag agg	acg act gga aat	tca atc cat caa	gca caa gac ggt		1392		
3786	Glu Leu Gln Arg	Thr Thr Gly Asn	Ser Ile His Gln	Ala Gln Asp Gly				
3787		450		455		460		
3789	aca acc act aca	gct cct tat ggt	gac tcc ttg ctg	agc gag gag gtt		1440		
3790	Thr Thr Thr Thr	Ala Pro Tyr Gly	Asp Ser Leu Leu	Ser Glu Glu Val				
3791		465		470		475		480
3793	gca agt gca ctt	gcg gaa ctc ctc	ccc gta tgg tct	cag ctg atc gaa		1488		
3794	Ala Ser Ala Leu	Ala Glu Leu Leu	Pro Val Trp Ser	Gln Leu Ile Glu				
3795		485		490		495		
3797	gag cat agc ctt	caa gac ctc aag	gcg agc cct cag	gcg aag cgg ctc		1536		
3798	Glu His Ser Leu	Gln Asp Leu Lys	Ala Ser Pro Gln	Ala Lys Arg Leu				
3799		500		505		510		

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3801	gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct	1584
3802	Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro	
3803	515 520 525	
3805	gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg	1632
3806	Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val	
3807	530 535 540	
3809	gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt	1680
3810	Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser	
3811	545 550 555 560	
3813	gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag	1728
3814	Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln	
3815	565 570 575	
3817	tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca	1776
3818	Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser	
3819	580 585 590	
3821	aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa	1824
3822	Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu	
3823	595 600 605	
3825	att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc	1872
3826	Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala	
3827	610 615 620	
3829	gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat	1920
3830	Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr	
3831	625 630 635 640	
3833	ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg	1968
3834	Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu	
3835	645 650 655	
3837	gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg	2016
3838	Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp	
3839	660 665 670	
3841	gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg	2064
3842	Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser	
3843	675 680 685	
3845	agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat	2112
3846	Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp	
3847	690 695 700	
3849	cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag	2160
3850	Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys	
3851	705 710 715 720	
3853	tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa	2208
3854	Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln	
3855	725 730 735	
3857	ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc	2256
3858	Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala	
3859	740 745 750	
3861	aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct	2304
3862	Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala	
3863	755 760 765	
3865	ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg	2352

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3866	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	
3867		770					775					780					
3869	ctc	aga	acg	ccg	ttc	aag	agt	ggt	cat	ttc	ggt	gga	acg	gag	acg	tct	2400
3870	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	
3871	785					790					795					800	
3873	tta	ggt	tgg	aaa	ggg	tat	atg	gaa	ggg	gcc	ata	cga	tcg	ggt	caa	cga	2448
3874	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	
3875					805					810					815		
3877	ggt	gct	gca	gaa	ggt	gtg	gct	agc	ctg	gtg	cca	gca	gca	tag			2490
3878	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala				
3879				820					825								

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Use of <220> Feature (NEW RULES):

Sequence(s) are missing the &lt;220&gt; Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#: ~~18, 20, 21~~ 25, ~~26~~ 27, ~~28~~ 29, ~~30~~ 31, ~~32~~ 33

↓  
see p. 7 for example

---

10/624, 6/9 ?

<210> 25

<211> 1000

<212> PRT

<213> Unknown

no explanation given

<220>

<221> SIGNAL

<222> (1)... (24)

<400> 25



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Input Set : A:\0875CSEQUENCE LISTING.txt

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L:17 M:270 C: Current Application Number differs, Replaced Current Application No  
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:43 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:300  
L:284 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:287 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:552 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10  
L:799 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16  
L:1041 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18  
L:1045 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18  
L:1049 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18  
L:1340 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20  
L:1347 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1348 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1350 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20  
L:1354 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20  
L:1813 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:1817 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24  
L:1821 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24  
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L:1829 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24  
L:1832 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24  
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L:2099 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:25, <213>  
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L:2099 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:25,Line#:2099  
L:2237 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:2241 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26  
L:2245 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26  
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L:2520 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:27, <213>  
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L:2520 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:2520  
L:2657 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:2660 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28  
L:2664 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28  
L:2668 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28  
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L:2991 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:29, <213>  
ORGANISM:Unknown  
L:2991 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:29, <213>  
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L:2991 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:2991  
L:3155 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:3156 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:3158 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:3162 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30  
L:3166 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30

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Input Set : A:\0875CSEQUENCE LISTING.txt

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L:3170 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30  
L:3174 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30  
L:3177 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30  
L:3181 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30  
L:3488 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:31, <213>  
ORGANISM:Unknown  
L:3488 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:31, <213>  
ORGANISM:Unknown  
L:3488 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:31, Line#:3488  
L:3651 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER  
L:3653 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:3656 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32  
L:3660 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32  
L:3664 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32  
L:3668 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32  
L:3672 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32  
L:3887 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:33, <213>  
ORGANISM:Unknown